AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1 (Currently Amended). A screening method for simultaneous detection of diarrheagenic *Shigella* species and *E. coli* (DEC) ~~including~~ selected from the group consisting of one or more of Attaching and Effacing *E. coli* (A/EEC), ~~&~~ Enteropathogenic *E. coli* (EPEC), Enterotoxigenic *E. coli* (ETEC), Verocytotoxin-producing *E. coli* (VTEC), Enteroinvasive *E. coli* (EIEC) and strains ~~with~~ containing the *ehxA* gene, wherein said method comprises

performing multiplex PCR by contacting a sample with ~~two or more~~ multiple primers in a single reaction, wherein the multiple primers comprise at least one primer which specifically amplifies ~~*exhA*~~ *vtx1* or a part thereof, at least one primer that specifically amplifies *vtx2* or a part thereof, at least one primer that specifically amplifies *ipaH* or a part thereof, at least one primer that specifically amplifies *eae* or a part thereof, at least one primer that specifically amplifies *estA* or *sta* or a part thereof, and at least one primer that specifically amplifies *elt* or a part thereof,

~~at least a second primer selected from a primer which specifically amplifies *vtx1*, or a primer which specifically amplifies *vtx2*,~~

~~and at least one primer which specifically amplifies a further gene selected from the group consisting of: *ipaH, eae, sta* or *estA, vtx1, vtx2* and *elt*,~~

wherein ~~at least one of~~ the primers are each independently selected from the group consisting of:

a) the primers listed in Table 3;

b) sequences having a sequence identity of at least 80% with a primer listed in Table 3; and

c) a fragment of a primer listed in Table 3 comprising at least 10 nucleotides;

detecting the presence of the one or more amplified genes; and identifying subjects having the amplified ~~*ehxA* and *vtx1* or *vtx2*~~ genes.

Claims 2 – 38 (Canceled).

39 (Currently Amended). The screening method according to claim 1, further comprising amplifying and detecting one or both of the genes ~~comprising~~ consisting of: *ehxA* and *bfpA* ~~*ipaH, eae, sta, vtx1, vtx2,* and *elt,* parts of these genes or products of these genes~~ or parts thereof~~, such as RNA or polypeptides~~.

40 (Canceled).

41 (Previously Presented). The screening method according to claim 1 wherein the genes are detected by size identification.

42 (Previously Presented). The screening method according to claim 41 wherein the means for detecting by size identification is performed by agarose gel electrophoresis or capillary electrophoresis.

43 (Previously Presented). The screening method according to claim 1 wherein the genes are detected with a hybridization probe for each of the amplified genes.

44 (Previously Presented). The screening method according to claim 43 wherein the probes are selected from table 7.

45 (Currently Amended). The screening method according to claim 1 wherein the ~~material~~sample to be analyzed is selected from the group consisting of stool samples, consumables, bacterial cultures, and sewage samples.

46 (Previously Presented). The screening method according to claim 45, in which the testing is carried out on a sample from a human or an animal or from food or beverages.

47 (Canceled).

48 (Currently Amended). The screening method according to claim ~~47~~1 wherein said primers consist of 14, 15, 16, 17, 18, 19, 20, 21 or 22 consecutive nucleotides.

49 (Currently Amended). The screening method according to claim ~~47~~1 wherein said primers consist of ~~at most~~ 90, 80, 70, 60, 50, 40, or 30 nucleotides.

50 (Currently Amended). The screening method according to claim 43, in which the sequences are detected using two or more probes each independently selected from the group consisting of:

i) the probe sequences of table 7;

~~b)~~ii) sequences having a sequence identity of at least 80% with the ~~primer~~ probe sequences of ~~a)~~ii);

~~c)~~iii) parts of the sequences in ~~a) or b)~~ i) or ii), having a length of more than 10~~, preferable more than 16 nucleotides, such as more than 17, 18, 19 or 20~~ nucleotides;

~~d)~~iv) sequences comprising a sequence in ~~a), b) or c)~~ i), ii) or iii), said sequence having a length of no more than 100 nucleotides.

51 (Currently Amended). The screening method according to claim 50 wherein said probes have at least 85%~~, 90%, or 95%~~ sequence identity with the sequences of ~~a)~~ i).

52 (Currently Amended). The screening method according to claim 50 wherein said probes consist of 14, 15, 16, 17, 18, 19, 20, 21 or 22 consecutive nucleotides of the sequences in ~~a) or b)~~ i) or ii).

53 (Currently Amended). The screening method according to claim 50 wherein said probes consist of ~~at most~~ 90, 80, 70, 60, 50, 40, or 30 nucleotides of the sequences comprising ~~a), b), or c)~~i), ii) or iii).

54 (Currently Amended). A kit which comprises, in a single or in separate containers, nucleotide sequences which are able to prime amplify, in a nucleotide sequence amplification reaction, the genes: *ipaH, eae, estA, vtx1, vtx2,* and *elt* or parts of these genes or the complementary strands to the genes or parts thereof wherein the nucleotide sequences for priming are selected from the group consisting of the priming sequences in table 3 or sequences having at least 80% identity with the priming sequences in table 3 and which comprises a control.

55 (Previously Presented). The kit according to claim 54 wherein the sequence amplification reaction is PCR.

56 (Previously Presented). The kit according to claim 54 wherein the control consists of primers for 16s rDNA.

57 (Canceled).

58 (Currently Amended). The kit according to claim 54 further comprising probes for detecting each of the amplified genes, wherein the nucleotide sequences for probing are selected from the group consisting of the probe sequences in table 7.

59 (Previously Presented). The kit according to claim 54 which comprises a means for detecting by size identification.

60 (Previously Presented). The kit according to claim 59 wherein the means for detecting by size identification is performed by agarose gel electrophoresis or capillary electrophoresis.

61 (New). The screening method according to claim 1, wherein the performing multiplex PCR step further comprises primers which amplify a control sequence.

62 (New). The screening method according to claim 61, wherein the control sequence is 16s rDNA.

63 (New). The screening method according to claim 1, wherein the primers are selected from the primers listed in Table 3.